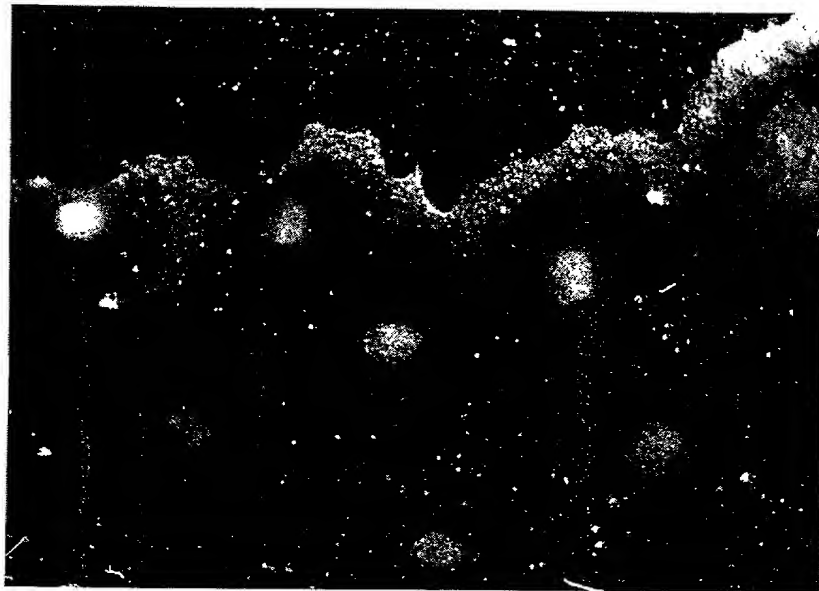
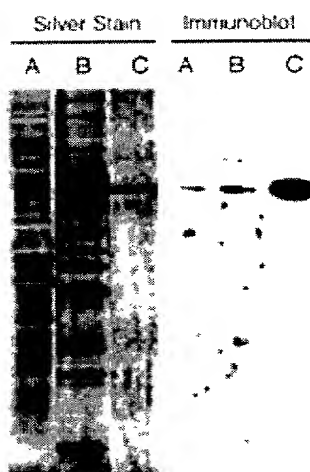


Figure 1



Bcap73 localizes to the forefront of endothelial cells migrating in response to injury.

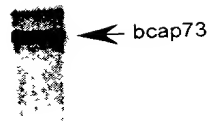
Figure 2



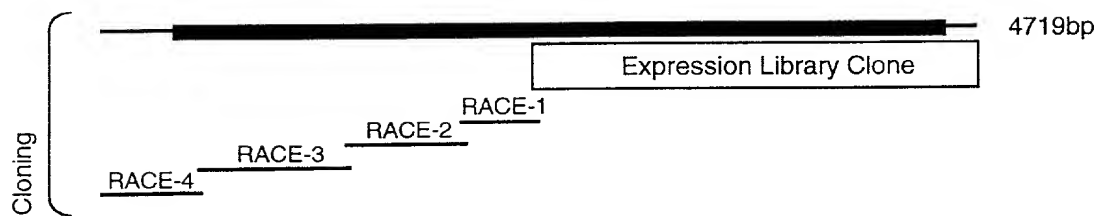
Bcap73 purification by ion-exchange chromatography.

Figure 3

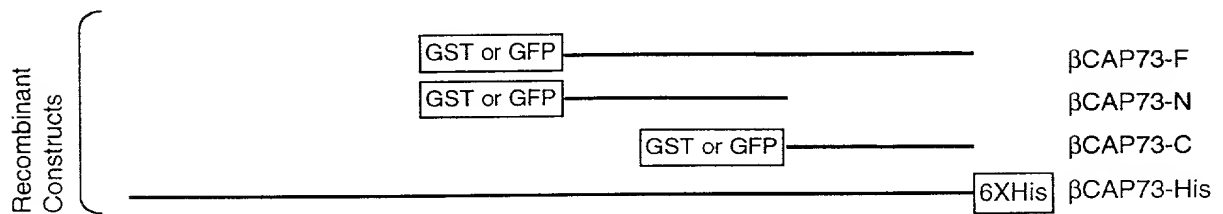
A



B



C



D

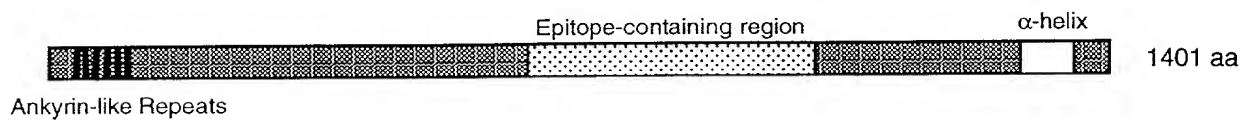


Figure 4-1

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ggggctgctc ttaatcaagt gctgccgctg caaggaagat aattttcaag cgttatgaag 180
gcggagaagg attccgaaga cgaagaaaaat atccttagag atccaagcta agtgtagtgc 240
agcatgaaga ttgcagaaca ggaagagttc taagaagaag gactgagtca ctagtttagga 300
gtctctctga gggctggctt tgtgagccac agtgatttgt aacttaatgc gaactaattt 360
gctgttagca acaagaaact aaatcctgtc t atg atg agc tgt tgg ttt tct 412
                               Met Met Ser Cys Trp Phe Ser
                               1                               5

tgt gct cct aag aac aga caa gca gca gat tgg aac aaa tac gat gac 460
Cys Ala Pro Lys Asn Arg Gln Ala Ala Asp Trp Asn Lys Tyr Asp Asp
                               10                               20

cga ttg atg aga gca gca gaa agg gga gat gta gaa aaa gtg tcc tca 508
Arg Leu Met Arg Ala Ala Glu Arg Gly Asp Val Glu Lys Val Ser Ser
                               25                               30                               35

atc ctt gct aaa aag gga gtc aat cca ggc aag cta gat gta gaa ggc 556
Ile Leu Ala Lys Lys Gly Val Asn Pro Gly Lys Leu Asp Val Glu Gly
                               40                               45                               50                               55

aga tct gcc ttt cat gtt gtg gcc tca aag gga aat ctt gag tgt ttg 604
Arg Ser Ala Phe His Val Val Ala Ser Lys Gly Asn Leu Glu Cys Leu
                               60                               65                               70

aat gcc atc ctc ata cat gga gtt gat att aca acc agt gac acc gca 652
Asn Ala Ile Leu Ile His Gly Val Asp Ile Thr Thr Ser Asp Thr Ala
                               75                               80                               85

gga agg aat gct ctt cac ctg gct gca aag tat ggg cat gca ctg tgt 700
Gly Arg Asn Ala Leu His Leu Ala Ala Lys Tyr Gly His Ala Leu Cys
                               90                               95                               100

cta caa aaa ctt cta cag tac aat tgt ccc act gaa cat gta gac ctg 748
Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro Thr Glu His Val Asp Leu
                               105                               110                               115

cag gga aga act gca ctt cat gat gca gct atg gca gac tgt cct tct 796
Gln Gly Arg Thr Ala Leu His Asp Ala Ala Met Ala Asp Cys Pro Ser
                               120                               125                               130                               135

agc ata cag ctg ctc tgc gac cat ggg gcc tcg gtg aat gcc aaa gat 844
Ser Ile Gln Leu Leu Cys Asp His Gly Ala Ser Val Asn Ala Lys Asp
                               140                               145                               150

```

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

Figure 4-3

ttt aag tat ttt gag agt gat cat tta gga tca gga agt cat ttc agg	1516
Phe Lys Tyr Phe Glu Ser Asp His Leu Gly Ser Gly Ser His Phe Arg	
360 365 370 375	
aaa gaa gat atg ctt ctt aaa caa ggt caa atg tac atg aca gac tca	1564
Lys Glu Asp Met Leu Leu Lys Gln Gly Gln Met Tyr Met Thr Asp Ser	
380 385 390	
cag tgt act tcc aca ggc atg cca gtc cat atg caa agc cga tct atg	1612
Gln Cys Thr Ser Thr Gly Met Pro Val His Met Gln Ser Arg Ser Met	
395 400 405	
tta aga cca ctg gag cta gcc tta cct aat caa gcc tca tat tcg gaa	1660
Leu Arg Pro Leu Glu Leu Ala Leu Pro Asn Gln Ala Ser Tyr Ser Glu	
410 415 420	
aac gaa att tta aag aaa gaa tta gaa gca atg aga act ttc tgt gat	1708
Asn Glu Ile Leu Lys Lys Glu Leu Glu Ala Met Arg Thr Phe Cys Asp	
425 430 435	
tca gca aaa caa gac aga ctc aaa ctc caa aat gaa ctg gct cac aag	1756
Ser Ala Lys Gln Asp Arg Leu Lys Leu Gln Asn Glu Leu Ala His Lys	
440 445 450 455	
gtg gcg gag tgc aag gcc tta gca ttg gaa tgt gaa agg gtg aaa gag	1804
Val Ala Glu Cys Lys Ala Leu Ala Leu Glu Cys Glu Arg Val Lys Glu	
460 465 470	
gat tca gat gag cag ata aag caa cta gaa gat gcc ttg aaa gac gtg	1852
Asp Ser Asp Glu Gln Ile Lys Gln Leu Glu Asp Ala Leu Lys Asp Val	
475 480 485	
cag aag aga atg tat gag tcg gaa ggt aaa gtg aaa caa atg cag aca	1900
Gln Lys Arg Met Tyr Glu Ser Glu Gly Lys Val Lys Gln Met Gln Thr	
490 495 500	
cat ttt ctt gcc ttg aaa gag cac ctg aca agt gat gcg gcc act ggg	1948
His Phe Leu Ala Leu Lys Glu His Leu Thr Ser Asp Ala Ala Thr Gly	
505 510 515	
aac cac agg ctg atg gag gaa ctg aag gat cag ttg aaa gac atg aaa	1996
Asn His Arg Leu Met Glu Glu Leu Lys Asp Gln Leu Lys Asp Met Lys	
520 525 530 535	
gtg aaa tac gaa ggt gcg tcc gca gaa gtg ggg aaa ttg aga aac caa	2044
Val Lys Tyr Glu Gly Ala Ser Ala Glu Val Gly Lys Leu Arg Asn Gln	
540 545 550	
atc aaa caa aat gaa atg tta gtt gaa gag ttt aag aga gat gag ggc	2092
Ile Lys Gln Asn Glu Met Leu Val Glu Glu Phe Lys Arg Asp Glu Gly	
555 560 565	

1000 900 800 700 600 500 400 300 200 100 0

Figure 4-4

aag ctg atg gaa gag aat aag cga ctg cag aag gag ttg agc atg tgt	2140
Lys Leu Met Glu Glu Asn Lys Arg Leu Gln Lys Glu Leu Ser Met Cys	
570 575 580	
 gaa ctg gag cga gag aag aga gga agg aag ctc act gag atg gaa ggc	2188
Glu Leu Glu Arg Glu Lys Arg Gly Arg Lys Leu Thr Glu Met Glu Gly	
585 590 595	
 cag tta aag gac ttg tca gcc aag ctg gcc ctt tct att cca gca gag	2236
Gln Leu Lys Asp Leu Ser Ala Lys Leu Ala Leu Ser Ile Pro Ala Glu	
600 605 610 615	
 aaa ttt gaa aac atg aag agc ttg tta tca aat gaa ctg aac gag aag	2284
Lys Phe Glu Asn Met Lys Ser Leu Leu Ser Asn Glu Leu Asn Glu Lys	
620 625 630	
 gca aaa aaa tta ata gat gtg gaa aga gaa tat gaa aga tca ctt aat	2332
Ala Lys Lys Leu Ile Asp Val Glu Arg Glu Tyr Glu Arg Ser Leu Asn	
635 640 645	
 gaa act aga cca tta aag aga gaa ctt gag aat ttg aag gcc aaa ctg	2380
Glu Thr Arg Pro Leu Lys Arg Glu Leu Glu Asn Leu Lys Ala Lys Leu	
650 655 660	
 gct cag cac gtc aaa cca gag gaa cat gag cag ctc aag agc aga tta	2428
Ala Gln His Val Lys Pro Glu Glu His Glu Gln Leu Lys Ser Arg Leu	
665 670 675	
 gag cag aag tca gga gaa ctt ggg aag agg atc act gag tta aca tcg	2476
Glu Gln Lys Ser Gly Glu Leu Gly Lys Arg Ile Thr Glu Leu Thr Ser	
680 685 690 695	
 aaa aat cag acg tta caa aag gaa atc gaa aag gtc tgc ctg gat aat	2524
Lys Asn Gln Thr Leu Gln Lys Glu Ile Glu Lys Val Cys Leu Asp Asn	
700 705 710	
 aag ctc ctt aca caa caa gta aat aac tta aca act gaa atg aaa aat	2572
Lys Leu Leu Thr Gln Gln Val Asn Asn Leu Thr Thr Glu Met Lys Asn	
715 720 725	
 cat tac gtc cct tta aaa gta agt gaa gaa atg aaa aag tca cat gat	2620
His Tyr Val Pro Leu Lys Val Ser Glu Glu Met Lys Lys Ser His Asp	
730 735 740	
 gta att gtt gat gat ttg aat aaa aag ctt tca gat gtg aca cac aaa	2668
Val Ile Val Asp Asp Leu Asn Lys Lys Leu Ser Asp Val Thr His Lys	
745 750 755	
 tat aca gaa aag aag ttg gaa atg gag aag ttg ctt atg gaa aat gcc	2716
Tyr Thr Glu Lys Lys Leu Glu Met Glu Lys Leu Leu Met Glu Asn Ala	
760 765 770 775	

Figure 4-5

agt tta agt aaa aat gtc agc cgc ctg gaa act gtg ttc ata cct ccc	2764
Ser Leu Ser Lys Asn Val Ser Arg Leu Glu Thr Val Phe Ile Pro Pro	
780 785 790	
gag aga cac gaa aaa gaa atg atg gct ctg aaa tcc aat atc act gaa	2812
Glu Arg His Glu Lys Glu Met Met Ala Leu Lys Ser Asn Ile Thr Glu	
795 800 805	
ctt aag aag cag ctg tct gaa ctt aat aaa aaa tgt ggt gaa gac caa	2860
Leu Lys Lys Gln Leu Ser Glu Leu Asn Lys Lys Cys Gly Glu Asp Gln	
810 815 820	
gag aaa ata tat tca ctc atg tct gaa aac aat gat ttg aaa aag acc	2908
Glu Lys Ile Tyr Ser Leu Met Ser Glu Asn Asn Asp Leu Lys Lys Thr	
825 830 835	
atg agt cat cag tat gtg ccc gtg aaa acc cat gaa gag att aaa act	2956
Met Ser His Gln Tyr Val Pro Val Lys Thr His Glu Glu Ile Lys Thr	
840 845 850 855	
gcc ttg agt agc aca ttg gat aaa acc aat aga gaa tta gta gat gtg	3004
Ala Leu Ser Ser Thr Leu Asp Lys Thr Asn Arg Glu Leu Val Asp Val	
860 865 870	
aag aag aag tgt gaa gat ata aat caa gaa ttt gtg aaa ata aaa gat	3052
Lys Lys Lys Cys Glu Asp Ile Asn Gln Glu Phe Val Lys Ile Lys Asp	
875 880 885	
gag aac gaa ata tta aaa aga aat ctg gag aac act cag aac caa gta	3100
Glu Asn Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln Asn Gln Val	
890 895 900	
aaa gct gag tac atc agc cta aga gag cat gaa gaa aag atg agt ggc	3148
Lys Ala Glu Tyr Ile Ser Leu Arg Glu His Glu Glu Lys Met Ser Gly	
905 910 915	
cta agg aag agc atg aag aag gtc cag gac aac agc gct gaa ata ctg	3196
Leu Arg Lys Ser Met Lys Lys Val Gln Asp Asn Ser Ala Glu Ile Leu	
920 925 930 935	
gct aag tac aaa aaa agc cag gag gag att gtc acc ctg cat gag gag	3244
Ala Lys Tyr Lys Lys Ser Gln Glu Glu Ile Val Thr Leu His Glu Glu	
940 945 950	
att gca gcc cag aag aga gaa ctc gac acg ata cag gaa tgc atc aag	3292
Ile Ala Ala Gln Lys Arg Glu Leu Asp Thr Ile Gln Glu Cys Ile Lys	
955 960 965	
cta aaa tat gct ccg atc atc agc ttg gaa gag tgt gag aga aaa ttt	3340
Leu Lys Tyr Ala Pro Ile Ile Ser Leu Glu Glu Cys Glu Arg Lys Phe	
970 975 980	

The amino acid sequence of the protein encoded by the cDNA was determined by mass spectrometry. The sequence is identical to that of the protein encoded by the cDNA.

Figure 4-6

aaa gcc act gag aaa gaa cta aaa gaa cag cta tcc cag cag aca cag	3388
Lys Ala Thr Glu Lys Glu Leu Lys Glu Gln Leu Ser Gln Gln Thr Gln	
985 990 995	
aag tat aat acc agt gaa gaa gag gcc aag aag tgc aag caa gag aat	3436
Lys Tyr Asn Thr Ser Glu Glu Glu Ala Lys Lys Cys Lys Gln Glu Asn	
1000 1005 1010 1015	
gac aag tta aag aag gag atc ctc act ctt cag aag gat cta aag gat	3484
Asp Lys Leu Lys Lys Glu Ile Leu Thr Leu Gln Lys Asp Leu Lys Asp	
1020 1025 1030	
aag aat gtt cac att gag aat tct tat gaa aca gaa aga gca tta agc	3532
Lys Asn Val His Ile Glu Asn Ser Tyr Glu Thr Glu Arg Ala Leu Ser	
1035 1040 1045	
aga aaa aca gaa gag ctg aac aga cag tta aaa gac ctg ttg cag aaa	3580
Arg Lys Thr Glu Glu Leu Asn Arg Gln Leu Lys Asp Leu Leu Gln Lys	
1050 1055 1060	
tac aca gag gca aag aag gag aaa gag aag ctc gtg gag gaa aat gcc	3628
Tyr Thr Glu Ala Lys Lys Glu Lys Glu Lys Leu Val Glu Glu Asn Ala	
1065 1070 1075	
aag cag act tct gag atc ctt gca gca caa act ctt ttg cag aag cag	3676
Lys Gln Thr Ser Glu Ile Leu Ala Ala Gln Thr Leu Leu Gln Lys Gln	
1080 1085 1090 1095	
cat gtt ccg ctg gag cag gtt gag tcc ctg aaa aaa tct ctt agt ggt	3724
His Val Pro Leu Glu Gln Val Glu Ser Leu Lys Lys Ser Leu Ser Gly	
1100 1105 1110	
aca atc gag aca ctc aag gaa gaa ctg aaa act aag cag aga tgt tat	3772
Thr Ile Glu Thr Leu Lys Glu Glu Leu Lys Thr Lys Gln Arg Cys Tyr	
1115 1120 1125	
gag aaa gag cag cag aca gtg acc caa ctg cgg cag atg ctg gag aat	3820
Glu Lys Glu Gln Gln Thr Val Thr Gln Leu Arg Gln Met Leu Glu Asn	
1130 1135 1140	
cag aag aac tcc tct gtg ccc ctg gct gag cat ttg cag gtt aag gaa	3868
Gln Lys Asn Ser Ser Val Pro Leu Ala Glu His Leu Gln Val Lys Glu	
1145 1150 1155	
gca ttt gag aaa gaa gtt gga atc ata aaa gct agc ttg aga gaa aag	3916
Ala Phe Glu Lys Glu Val Gly Ile Ile Lys Ala Ser Leu Arg Glu Lys	
1160 1165 1170 1175	
gaa gaa gaa agc caa aac aaa act gaa gag gtc tcc aaa ctc cag tct	3964
Glu Glu Glu Ser Gln Asn Lys Thr Glu Glu Val Ser Lys Leu Gln Ser	
1180 1185 1190	

1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190

Figure 4-7

gag att cag aat act aaa caa gcg tta aaa aaa tta gag act cgg gag	4012
Glu Ile Gln Asn Thr Lys Gln Ala Leu Lys Lys Leu Glu Thr Arg Glu	
1195 1200 1205	
gtg gtt gat ttg tcg aaa tat aaa gca acg aaa agc gat ttg gag aca	4060
Val Val Asp Leu Ser Lys Tyr Lys Ala Thr Lys Ser Asp Leu Glu Thr	
1210 1215 1220	
cag att tcc gac tta aac gaa aaa ttg gcc aat ctg aat agg aag tat	4108
Gln Ile Ser Asp Leu Asn Glu Lys Leu Ala Asn Leu Asn Arg Lys Tyr	
1225 1230 1235	
gag gaa gta tgt gag gag gtt ttg cat gcc aaa aag aag gaa ctg tct	4156
Glu Glu Val Cys Glu Glu Val Leu His Ala Lys Lys Lys Glu Leu Ser	
1240 1245 1250 1255	
gct aaa gat gag aag gaa ttg ctc cat ttc agc ata gag caa gaa atc	4204
Ala Lys Asp Glu Lys Glu Leu Leu His Phe Ser Ile Glu Gln Glu Ile	
1260 1265 1270	
aaa gat cag cag gaa cga tgt gac aaa tcc tta aca acc atc acg gag	4252
Lys Asp Gln Gln Glu Arg Cys Asp Lys Ser Leu Thr Thr Ile Thr Glu	
1275 1280 1285	
cta cag aga aga ata cag gaa tct gcc aaa caa atc gaa gca aaa gat	4300
Leu Gln Arg Arg Ile Gln Glu Ser Ala Lys Gln Ile Glu Ala Lys Asp	
1290 1295 1300	
aat aag ata act gaa ctg ctc aat gat gtg gag aga tta aaa cag gcc	4348
Asn Lys Ile Thr Glu Leu Leu Asn Asp Val Glu Arg Leu Lys Gln Ala	
1305 1310 1315	
ctc aat ggc ctt tcc cag ctc acc tat gga agt ggg agt ccc agc aag	4396
Leu Asn Gly Leu Ser Gln Leu Thr Tyr Gly Ser Gly Ser Pro Ser Lys	
1320 1325 1330 1335	
agg cag agt cag ctg att gac agc ctg cag cag cag gtc agg tcc ctg	4444
Arg Gln Ser Gln Leu Ile Asp Ser Leu Gln Gln Gln Val Arg Ser Leu	
1340 1345 1350	
cag cag cag ctg gcg gat gcc gac aga cag cac caa gaa gta att gca	4492
Gln Gln Gln Leu Ala Asp Ala Asp Arg Gln His Gln Glu Val Ile Ala	
1355 1360 1365	
att tat cgg aca cac ctt ctt agt gct gca cag ggt cac atg gat gag	4540
Ile Tyr Arg Thr His Leu Leu Ser Ala Ala Gln Gly His Met Asp Glu	
1370 1375 1380	
gat gtg cag gcc gcc tta ctg cag atc ata cag atg cgg cag ggg ctc	4588
Asp Val Gln Ala Ala Leu Leu Gln Ile Ile Gln Met Arg Gln Gly Leu	
1385 1390 1395	

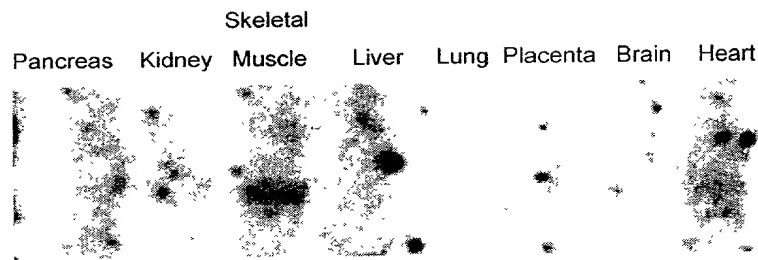
Figure 4-8

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gtg tgc tagtcggcac cccccagccc acagtggctt tccctgctgg tgctgagcat 4644
Val Cys
1400

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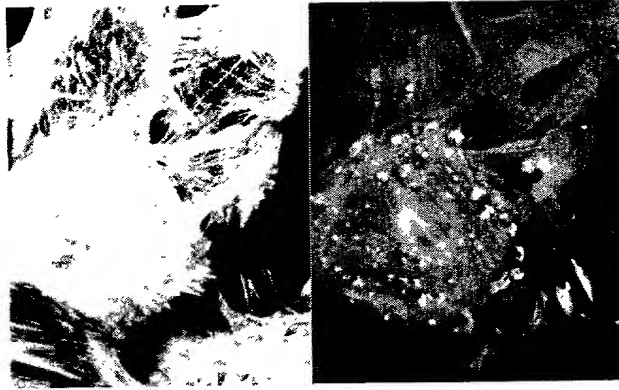
gtattttgat ccatcaaaaa aaaaaaaaaa aa 4736
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Figure 5



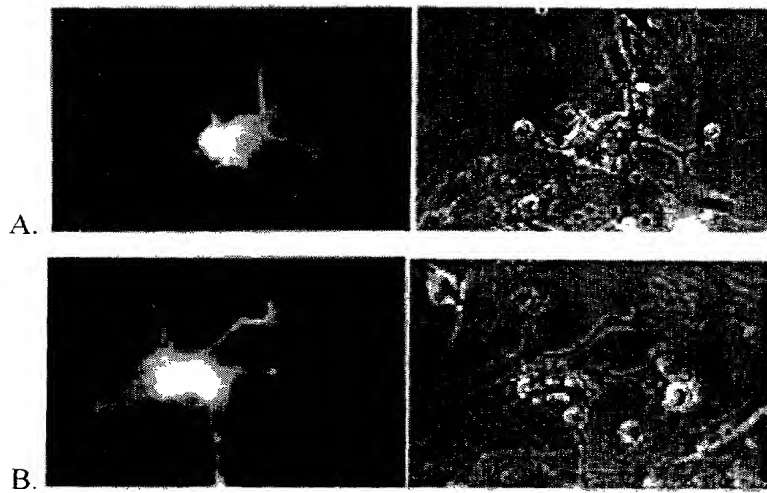
Bcap73 mRNA is expressed in various human tissues

Figure 6



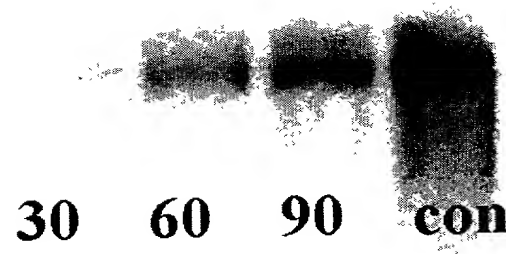
Overexpression of recombinant bcap73 induces formation of novel membrane protrusions

Figure 7



Overexpression of bcap73 domains induces aberrant cellular projections

Figure 8



Bcap73 mRNA is down-regulated in response to injury

Figure 9-2

Query: 898 atgtcaactgctgatagatagagggcgcatattaattccagagacaaacaaaacaggac 957
|||||
Sbjct: 552 ctgtcaactgctgatagatcgagggcgagagattaattccagagacaaacaaaacagaac 611

Query: 958 tgctctcatgctaggatgagagtatgggtgcaaagatgcagtagaagtcttaatacaaaaa 1017
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Query: 1078 tggtgacaatctggacattctaacttactgaagactgcatcagaaaaattccaacaaagg 1137
|||||
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Query: 1138 gagagaactttggaagaaaggaccatctttacaacagcgaaatttgctcagatgctaga 1197
|||||
Sbjct: 792 gagagaactttggaagaaaggaccatctttacagcagcgaaatttgccgtacatgctaga 851

Query: 1198 tgaagtaaatacgaagtcaaatacagaggagcatcaaacattcaggatctggagattga 1257
|||||
Sbjct: 852 tgaagtaaattggaagtaagtcagaggagcatcgaaacattcaggagctggagattga 911

Query: 1258 aaatgaagatctgaaagagagattgagaaaaattcagcaagaacagagaatattattgga 1317
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Figure 9-3

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Sbjct: 1376 actctgatgagcagataaagcagttagaagacgcattgaaagatgtgcagaagagaatgt 1435

Query: 1866 atgagtcggaaggtaaagtgaacaaatgcagacacattttctgccttgaaagagcacc 1925
|||||
Sbjct: 1436 atgagtcggaaggtaaagtgaacaaatgcagacacactttctgccttgaaagagcacc 1495

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Query: 2106 agaataagcgactgcagaaggagttgagcatgtgtgaaactggagcgagagaagagaggaa 2165
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Sbjct: 1676 agaataagcgattgcagaaggaaactcagtatgtgtgaaacggagcgagacaagaaaggaa 1735

Figure 9-4

Query: 2166 ggaagctcactgagatggaaggccagttaaaggacttgtcagccaagctggccctttcta 2225
 ||| | | ||||| ||||| ||||| ||||| | | ||| ||||| || | ||
Sbjct: 1736 ggaggggttgctgaggtggaaggccaggtaaaggaactcttagcaaagctgaccttgtcag 1795

Query: 2226 ttccagcagagaaatttgaaaacatgaagagcttggttatcaa 2267
 ||||| | || ||||| || | ||||| ||||| |||||
Sbjct: 1796 ttccaactgaaaaatttgagagcatgaagagcttattatcaa 1837

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Figure 10-1

Sequence Alignment of bcap73 against Tentative Human Concensus (THC) Contiguous Sequences
THC244788 THC143090 THC186491 THC213238 (from TIGR)

Score = 1052 bits (547), Expect = 0.0

Identities = 905/1092 (82%), Positives = 905/1092 (82%), Gaps = 4/1092 (0%)

Query=bcap73 cDNA

Sbjct=THC seq

Query: 3136 aaagatgagtggtcctaaggaagagcatgaagaaggtccaggacaacagcgctgaaatact 3195
||||||| ||||| ||||||||| ||||| ||||| | | ||||||||| |
Sbjct: 6 aaagatgagctcgctaagtcagagcatgagaaaggtscaggatagtaatgctgaaatctt 65

Query: 3196 ggctaagtacnnnnnnngccaggaggagattgtcacctgcatgaggagattgcagccca 3255
||| | ||| ||||| || ||||||||| || || ||||| || ||| |||||||
Sbjct: 66 ggccamctacagaaaaggccaagaagagattgtgacactkcatgccgaaattaragccca 125

Query: 3256 gaagagagaactcgacacgatacaggaatgcatcaagctaaaatatgctccgatcatcag 3315
|| || || ||||||||| ||||| || ||||||| || ||||||||| || || |||||
Sbjct: 126 gargarggagctcgacacaataacaagartgcattaaggtaaaaatatgccccattgtcag 185

Query: 3316 cttggaagagtgtgagagaaaatttaaagccactgagaaagaac-taaaagaacagctat 3374
||| || ||||| ||||||||| ||||||||| || ||||||||| ||||||||| ||| |||
Sbjct: 186 ctttgaggagtsctgagagaaaatttaaagcaacagagaaagaacctaaaagaccagttat 245

Query: 3375 cccagcagacacagaagtataataccagtgaagaagaggccaagaagtgaagcaagaga 3434
| ||||||||| ||||||||| | ||||||||| ||||||| ||||||||| |||
Sbjct: 246 cagagcagacacaaaagtatatgtgtcagtgaagaagaagtcaagaaaaacaagcaagaga 305

Query: 3435 atgacaagttaaagaaggagatcctcactcttcagaaggatctaaaggataagaatgttc 3494
||||||||| ||||||||| || || ||||||||| ||| | | ||||| |||||
Sbjct: 306 atgacaagttaaagaaggagatttttacccttcagaaagatttgagagayaagacagttc 365

Query: 3495 acattgagaattcttatgaacagaaagagcattaagcagaaaaacagaagagctgaaca 3554
||||||| || ||||||| ||||||||| ||||||||| ||||||||| ||||| |||||
Sbjct: 366 tcattgagaagtctcatgaaatggaaagagcattaagcagaaaaacagacgagctaaaca 425

Query: 3555 gacagttaaaagacctgttgcaaaatacacagaggcaaagaaggagaaagagaagctcg 3614
||||||||| ||| ||||||||| || || ||||||| || ||||||||| |||
Sbjct: 426 aacagttaaaagacttgtcacagaaatacacggaagtaagaatgtgaaagagaagctag 485

Symbol	Definition	Symbol	Definition
\mathbf{A}	Matrix	\mathbf{B}	Matrix
\mathbf{C}	Matrix	\mathbf{D}	Matrix
\mathbf{E}	Matrix	\mathbf{F}	Matrix
\mathbf{G}	Matrix	\mathbf{H}	Matrix
\mathbf{I}	Matrix	\mathbf{J}	Matrix
\mathbf{K}	Matrix	\mathbf{L}	Matrix
\mathbf{M}	Matrix	\mathbf{N}	Matrix
\mathbf{O}	Matrix	\mathbf{P}	Matrix
\mathbf{Q}	Matrix	\mathbf{R}	Matrix
\mathbf{S}	Matrix	\mathbf{T}	Matrix
\mathbf{U}	Matrix	\mathbf{V}	Matrix
\mathbf{W}	Matrix	\mathbf{X}	Matrix
\mathbf{Y}	Matrix	\mathbf{Z}	Matrix
\mathbf{a}	Vector	\mathbf{b}	Vector
\mathbf{c}	Vector	\mathbf{d}	Vector
\mathbf{e}	Vector	\mathbf{f}	Vector
\mathbf{g}	Vector	\mathbf{h}	Vector
\mathbf{i}	Vector	\mathbf{j}	Vector
\mathbf{k}	Vector	\mathbf{l}	Vector
\mathbf{m}	Vector	\mathbf{n}	Vector
\mathbf{o}	Vector	\mathbf{p}	Vector
\mathbf{q}	Vector	\mathbf{r}	Vector
\mathbf{s}	Vector	\mathbf{t}	Vector
\mathbf{u}	Vector	\mathbf{v}	Vector
\mathbf{w}	Vector	\mathbf{x}	Vector
\mathbf{y}	Vector	\mathbf{z}	Vector
\mathbf{A}^T	Transpose of \mathbf{A}	\mathbf{B}^T	Transpose of \mathbf{B}
\mathbf{C}^T	Transpose of \mathbf{C}	\mathbf{D}^T	Transpose of \mathbf{D}
\mathbf{E}^T	Transpose of \mathbf{E}	\mathbf{F}^T	Transpose of \mathbf{F}
\mathbf{G}^T	Transpose of \mathbf{G}	\mathbf{H}^T	Transpose of \mathbf{H}
\mathbf{I}^T	Transpose of \mathbf{I}	\mathbf{J}^T	Transpose of \mathbf{J}
\mathbf{K}^T	Transpose of \mathbf{K}	\mathbf{L}^T	Transpose of \mathbf{L}
\mathbf{M}^T	Transpose of \mathbf{M}	\mathbf{N}^T	Transpose of \mathbf{N}
\mathbf{O}^T	Transpose of \mathbf{O}	\mathbf{P}^T	Transpose of \mathbf{P}
\mathbf{Q}^T	Transpose of \mathbf{Q}	\mathbf{R}^T	Transpose of \mathbf{R}
\mathbf{S}^T	Transpose of \mathbf{S}	\mathbf{T}^T	Transpose of \mathbf{T}
\mathbf{U}^T	Transpose of \mathbf{U}	\mathbf{V}^T	Transpose of \mathbf{V}
\mathbf{W}^T	Transpose of \mathbf{W}	\mathbf{X}^T	Transpose of \mathbf{X}
\mathbf{Y}^T	Transpose of \mathbf{Y}	\mathbf{Z}^T	Transpose of \mathbf{Z}
\mathbf{a}^T	Transpose of \mathbf{a}	\mathbf{b}^T	Transpose of \mathbf{b}
\mathbf{c}^T	Transpose of \mathbf{c}	\mathbf{d}^T	Transpose of \mathbf{d}
\mathbf{e}^T	Transpose of \mathbf{e}	\mathbf{f}^T	Transpose of \mathbf{f}
\mathbf{g}^T	Transpose of \mathbf{g}	\mathbf{h}^T	Transpose of \mathbf{h}
\mathbf{i}^T	Transpose of \mathbf{i}	\mathbf{j}^T	Transpose of \mathbf{j}
\mathbf{k}^T	Transpose of \mathbf{k}	\mathbf{l}^T	Transpose of \mathbf{l}
\mathbf{m}^T	Transpose of \mathbf{m}	\mathbf{n}^T	Transpose of \mathbf{n}
\mathbf{o}^T	Transpose of \mathbf{o}	\mathbf{p}^T	Transpose of \mathbf{p}
\mathbf{q}^T	Transpose of \mathbf{q}	\mathbf{r}^T	Transpose of \mathbf{r}
\mathbf{s}^T	Transpose of \mathbf{s}	\mathbf{t}^T	Transpose of \mathbf{t}
\mathbf{u}^T	Transpose of \mathbf{u}	\mathbf{v}^T	Transpose of \mathbf{v}
\mathbf{w}^T	Transpose of \mathbf{w}	\mathbf{x}^T	Transpose of \mathbf{x}
\mathbf{y}^T	Transpose of \mathbf{y}	\mathbf{z}^T	Transpose of \mathbf{z}
\mathbf{A}^{-1}	Inverse of \mathbf{A}	\mathbf{B}^{-1}	Inverse of \mathbf{B}
\mathbf{C}^{-1}	Inverse of \mathbf{C}	\mathbf{D}^{-1}	Inverse of \mathbf{D}
\mathbf{E}^{-1}	Inverse of \mathbf{E}	\mathbf{F}^{-1}	Inverse of \mathbf{F}
\mathbf{G}^{-1}	Inverse of \mathbf{G}	\mathbf{H}^{-1}	Inverse of \mathbf{H}
\mathbf{I}^{-1}	Inverse of \mathbf{I}	\mathbf{J}^{-1}	Inverse of \mathbf{J}
\mathbf{K}^{-1}	Inverse of \mathbf{K}	\mathbf{L}^{-1}	Inverse of \mathbf{L}
\mathbf{M}^{-1}	Inverse of \mathbf{M}	\mathbf{N}^{-1}	Inverse of \mathbf{N}
\mathbf{O}^{-1}	Inverse of \mathbf{O}	\mathbf{P}^{-1}	Inverse of \mathbf{P}
\mathbf{Q}^{-1}	Inverse of \mathbf{Q}	\mathbf{R}^{-1}	Inverse of \mathbf{R}
\mathbf{S}^{-1}	Inverse of \mathbf{S}	\mathbf{T}^{-1}	Inverse of \mathbf{T}
\mathbf{U}^{-1}	Inverse of \mathbf{U}	\mathbf{V}^{-1}	Inverse of \mathbf{V}
\mathbf{W}^{-1}	Inverse of <		

Query: 4155 ctgctaaagatgagaaggaattgctccatttcagcatagagcaagaaatcaaagatcagc 4214
||| ||||||||||||| || | ||||| | | ||||| |||
Sbjct: 1025 ctgscaaagatgagaagga-ttactgc-tttcaccttgagscaggaaattaagggtcagr 1082

Figure 10-3

```
Query: 4215 aggaacgatgtg 4226
      |||||
Sbjct: 1083 aggaacgatgtg 1094
```

Figure 10-3 shows a sequence alignment between a query sequence (4215-4226) and a subject sequence (1083-1094). The alignment is perfect, with all 11 bases matching (aggaacgatgtg). The alignment is shown with vertical bars (|) indicating the matches.